

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. - 79. (Canceled)

80. (Currently Amended) A polypeptide consisting essentially of:

a first and second interactor domain and a circularly permuted β -lactamase protein where the first interactor domain is fused covalently bonded to a the circularly permuted β -lactamase protein through an the N-terminal breakpoint of the circularly permuted β -lactamase protein and a and the second interactor domain is fused covalently bonded to the circularly permuted β -lactamase protein through the a C-terminal breakpoint of the circularly permuted β -lactamase protein, wherein said circularly permuted β -lactamase protein is functionally reconstituted only upon binding of said first interactor domain and said second interactor domain to a single ligand.

81. - 83. (Canceled)

84. (Previously Presented) The polypeptide of claim 80, wherein said N-terminal break point and said C-terminal break point are within a solvent exposed loop between elements of secondary structure within the β -lactamase protein.

85. (Previously Presented) The polypeptide of claim 80, wherein said circularly permuted β -lactamase protein consists of amino acids 26 to 288 of the following sequence prior to circular permutation:

His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly
26				30				35					40		
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu

	45	50	55
Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys			
60	65	70	
Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu			
75	80	85	
Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr			
90	95	100	105
Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu			
110	115	120	
Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu			
125	130	135	
Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His			
140	145	150	
Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu			
155	160	165	
Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala			
170	175	180	185
Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu			
190	195	200	
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala			
205	210	215	
Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp			
220	225	230	
Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu			
235	240	245	
Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly			
250	255	260	265
Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly			

270 Ala Ser Leu Ile Lys His Trp
275
280
285

(SEQ ID NO: 2);

wherein said N-terminal breakpoint and said C-terminal breakpoint are within 10 amino acids of an amide bond junction between two amino acids selected from the group consisting of asparagine 52 and serine 53, leucine 91 and glycine 92, glutamine 99 and asparagine 100, proline 174 and asparagine 175, glutamic acid 197 and leucine 198, lysine 215 and valine 216, alanine 227 and glycine 228, and glycine 253 and lysine 254.

86. (Previously Presented) The polypeptide of claim 85, wherein said two amino acids are selected from the group consisting of proline 174 and asparagine 175, glutamic acid 197 and leucine 198, lysine 215 and valine 216, alanine 227 and glycine 228, and glycine 253 and lysine 254.

87. (Previously Presented) The polypeptide of claim 85, wherein said two amino acids are glutamic acid 197 and leucine 198.

88. (Previously Presented) The polypeptide of claim 80, wherein said ligand is a protein ligand.

89. (Canceled)